

# Murine scRNA-seq and data analyses

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 An abbreviated version of this protocol was published in Science Immunology in Apr 2023

Identification of a broadly fibrogenic macrophage subset induced by type 3 inflammation

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## Detailed protocol

The code needed to process the murine liver scRNAseq data, and to extract and annotate the monocyte/macrophage subset seen in Fig. 4A-D is available here: <https://github.com/alex-m-s-barron/mouseliver/commit/30ebb0357b4aed32a4fa4cb1511e68f636c3d935>. Code to generate the Nebulosa plot seen in Fig. 4A, the RNA Velocity plots in Fig. 4B-D and the image analysis in Fig. 4I are provided separately.

**How to cite:** (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Fabre, T. and Barron, A. M.(2023). Murine scRNA-seq and data analyses. Bio-protocol Preprint. [bio-protocol.org/prep2211](https://bio-protocol.org/prep2211).
2. Fabre, T., Barron, A. M., Christensen, S. M., Asano, S., Bound, K., Lech, M. P., Wadsworth, M. H., Chen, X., Wang, C., Wang, J., McMahon, J., Schlerman, F., White, A., Kravarik, K. M., Fisher, A. J., Borthwick, L. A., Hart, K. M., Henderson, N. C., Wynn, T. A. and Dower, K.(2023). Identification of a broadly fibrogenic macrophage subset induced by type 3 inflammation. Science Immunology 8(82). DOI: [10.1126/sciimmunol.add8945](https://doi.org/10.1126/sciimmunol.add8945)

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